

SEQUENCE LISTING

<110> Ishii, Yasuyuki
Yodoi, Junji
Nakamura, Hajime
Kondo, Norihiko

<120> Thioredoxin derivatives

<130> SAEG129.015APC

<140> 10/551,488

<141> 2005-09-29

<150> PCT/JP2004/004523

<151> 2004-03-30

<150> JP 2003-93342

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<150> JP 2003-349109

<151> 2003-08-10

<160> 14

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(318)

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Met	Val	Lys	Gln	Ile	Glu	Ser	Lys	Thr	Ala	Phe	Gln	Glu	Ala	Leu	Asp	
1			5						10					15		

gct	gca	ggt	gat	aaa	ctt	gta	gta	gtt	gac	ttc	tca	gcc	acg	tgg	tgt	96
Ala	Ala	Gly	Asp	Lys	Leu	Val	Val	Val	Asp	Phe	Ser	Ala	Thr	Trp	Cys	
			20					25					30			

ggg	cct	tgc	aaa	atg	atc	aag	cct	ttc	ttt	cat	tcc	ctc	tct	gaa	aag	144
Gly	Pro	Cys	Lys	Met	Ile	Lys	Pro	Phe	Phe	His	Ser	Leu	Ser	Glu	Lys	
		35					40					45				

tat	tcc	aac	gtg	ata	ttc	ctt	gaa	gta	gat	gtg	gat	gac	tgt	cag	gat	192
Tyr	Ser	Asn	Val	Ile	Phe	Leu	Glu	Val	Asp	Val	Asp	Asp	Cys	Gln	Asp	
	50					55					60					

gtt	gct	tca	gag	tgt	gaa	gtc	aaa	tgc	atg	cca	aca	ttc	cag	ttt	ttt	240
Val	Ala	Ser	Glu	Cys	Glu	Val	Lys	Cys	Met	Pro	Thr	Phe	Gln	Phe	Phe	
65					70				75					80		

aag	aag	gga	caa	aag	gtg	ggt	gaa	ttt	tct	gga	gcc	aat	aag	gaa	aag	288
Lys	Lys	Gly	Gln	Lys	Val	Gly	Glu	Phe	Ser	Gly	Ala	Asn	Lys	Glu	Lys	
			85						90					95		

ctt	gaa	gcc	acc	att	aat	gaa	tta	gtc	taa							318
Leu	Glu	Ala	Thr	Ile	Asn	Glu	Leu	Val								
			100					105								

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Met Val Lys Gln Ile Glu Ser Lys Thr Ala Phe Gln Glu Ala Leu Asp
 1 5 10 15

Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys
 20 25 30

Gly Pro Cys Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
 35 40 45

Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp
 50 55 60

Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
 65 70 75 80

Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
 85 90 95

Leu Glu Ala Thr Ile Asn Glu Leu Val
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gtcgacttag actaattcat taatggtggc

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 <223> nnn stands for any base for coding Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or Ph e.

<220>
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 <222> (1)..(318)
 <223> The 'Xaa' at location 35 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or Ph e.

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gct gca ggt gat aaa ctt gta gta gtt gac ttc tca gcc acg tgg tgt 96
Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys
20 25 30

ggg cct nnn aaa atg atc aag cct ttc ttt cat tcc ctc tct gaa aag 144
Gly Pro Xaa Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
35 40 45

tat tcc aac gtg ata ttc ctt gaa gta gat gtg gat gac tgt cag gat 192
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp
50 55 60

gtt gct tca gag tgt gaa gtc aaa tgc atg cca aca ttc cag ttt ttt 240
Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
65 70 75 80

aag aag gga caa aag gtg ggt gaa ttt tct gga gcc aat aag gaa aag 288
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
85 90 95

ctt gaa gcc acc att aat gaa tta gtc taa 318
Leu Glu Ala Thr Ile Asn Glu Leu Val
100 105

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1 5 10 15

gct gca ggt gat aaa ctt gta gta gtt gac ttc tca gcc acg tgg tgt 96
Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys
20 25 30

ggg cct tcc aaa atg atc aag cct ttc ttt cat tcc ctc tct gaa aag 144
Gly Pro Ser Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
35 40 45

tat tcc aac gtg ata ttc ctt gaa gta gat gtg gat gac tgt cag gat 192
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp
50 55 60

gtt gct tca gag tgt gaa gtc aaa tgc atg cca aca ttc cag ttt ttt 240
Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
65 70 75 80

aag aag gga caa aag gtg ggt gaa ttt tct gga gcc aat aag gaa aag 288
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys

	85	90	95	
ctt gaa gcc acc att aat gaa tta gtc taa				318
Leu Glu Ala Thr Ile Asn Glu Leu Val				
	100	105		

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<400> 13				
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Met Val Lys Gln Ile Glu Ser Lys Thr Ala Phe Gln Glu Ala Leu Asp				
1	5	10	15	

gct gca ggt gat aaa ctt gta gta gtt gac ttc tca gcc acg tgg tct				96
Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Ser				
	20	25	30	

ggg cct tcc aaa atg atc aag cct ttc ttt cat tcc ctc tct gaa aag				144
Gly Pro Ser Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys				
	35	40	45	

tat tcc aac gtg ata ttc ctt gaa gta gat gtg gat gac tgt cag gat				192
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp				
	50	55	60	

gtt gct tca gag tgt gaa gtc aaa tgc atg cca aca ttc cag ttt ttt				240
Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe				
65	70	75	80	

aag aag gga caa aag gtg ggt gaa ttt tct gga gcc aat aag gaa aag				288
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys				
	85	90	95	

ctt gaa gcc acc att aat gaa tta gtc taa				318
Leu Glu Ala Thr Ile Asn Glu Leu Val				
	100	105		

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Met Val Lys Gln Ile Glu Ser Lys Thr Ala Phe Gln Glu Ala Leu Asp				
1	5	10	15	

gct gca ggt gat aaa ctt gta gta gtt gac ttc tca gcc acg tgg tct				96
Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Ser				
	20	25	30	

ggg	cct	tgc	aaa	atg	atc	aag	cct	ttc	ttt	cat	tcc	ctc	tct	gaa	aag	144
Gly	Pro	Cys	Lys	Met	Ile	Lys	Pro	Phe	Phe	His	Ser	Leu	Ser	Glu	Lys	
		35					40					45				
tat	tcc	aac	gtg	ata	ttc	ctt	gaa	gta	gat	gtg	gat	gac	tgt	cag	gat	192
Tyr	Ser	Asn	Val	Ile	Phe	Leu	Glu	Val	Asp	Val	Asp	Asp	Cys	Gln	Asp	
	50					55					60					
gtt	gct	tca	gag	tgt	gaa	gtc	aaa	tgc	atg	cca	aca	ttc	cag	ttt	ttt	240
Val	Ala	Ser	Glu	Cys	Glu	Val	Lys	Cys	Met	Pro	Thr	Phe	Gln	Phe	Phe	
65					70					75				80		
aag	aag	gga	caa	aag	gtg	ggt	gaa	ttt	tct	gga	gcc	aat	aag	gaa	aag	288
Lys	Lys	Gly	Gln	Lys	Val	Gly	Glu	Phe	Ser	Gly	Ala	Asn	Lys	Glu	Lys	
				85					90					95		
ctt	gaa	gcc	acc	att	aat	gaa	tta	gtc	taa							318
Leu	Glu	Ala	Thr	Ile	Asn	Glu	Leu	Val								
			100					105								